GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 15:18:46 ; Search time 998 Seconds
(without alignments)
13059.814 Million cell updates/sec

Title: US-09-815-923-3
Perfect score: 1764
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8407786 seqs, 3694357880 residues

Total number of hits satisfying chosen parameters: 16815572

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1764 | 100.0 | 1764 | 2 | PCT-US02-08970-3 | Sequence 3, Appli |
| 2 | 579.8 | 32.9 | 2745 | 14 | US-10-144-771-11577 | Sequence 11577, A |
| 3 | 579.4 | 32.8 | 3190 | 15 | US-10-219-051B-13968 | Sequence 13968, A |
| 4 | 554.8 | 31.5 | 2964 | 18 | US-60-453-135-5294 | Sequence 5294, Ap |
| 5 | 554.8 | 31.5 | 2964 | 18 | US-60-453-050-5294 | Sequence 5294, Ap |
| 6 | 554.8 | 31.5 | 2964 | 19 | US-60-466-412-5294 | Sequence 5294, Ap |
| 7 | 552.4 | 31.3 | 2508 | 15 | US-10-219-051B-13970 | Sequence 13970, A |
| 8 | 552.4 | 31.3 | 2770 | 2 | PCT-US02-39565-43 | Sequence 43, Appl |
| 9 | 552.4 | 31.3 | 2964 | 11 | US-09-949-016-3430 | Sequence 3430, Ap |
| 10 | 552.4 | 31.3 | 2964 | 15 | US-10-170-235-38741 | Sequence 38741, A |
| 11 | 524 | 29.7 | 2342 | 18 | US-60-453-135-1580 | Sequence 1580, Ap |
| 12 | 524 | 29.7 | 2342 | 18 | US-60-453-050-1580 | Sequence 1580, Ap |
| 13 | 524 | 29.7 | 2342 | 19 | US-60-466-412-1580 | Sequence 1580, Ap |
| 14 | 522.4 | 29.6 | 1983 | 15 | US-10-219-051B-3166 | Sequence 3166, Ap |
| 15 | 522.4 | 29.6 | 1983 | 15 | US-10-219-051B-10901 | Sequence 10901, A |
| 16 | 522.4 | 29.6 | 2342 | 15 | US-10-170-235-25520 | Sequence 25520, A |
| 17 | 522.4 | 29.6 | 3405 | 15 | US-10-170-235-39744 | Sequence 39744, A |
| 18 | 522.4 | 29.6 | 3416 | 15 | US-10-170-235-39745 | Sequence 39745, A |
| 19 | 522.4 | 29.6 | 3554 | 15 | US-10-170-235-39639 | Sequence 39639, A |
| 20 | 513.6 | 29.1 | 2876 | 10 | US-09-724-676-47407 | Sequence 47407, A |
| 21 | 513.6 | 29.1 | 2876 | 10 | US-09-724-676A-47407 | Sequence 47407, A |
| 22 | 504.6 | 28.6 | 1863 | 2 | PCT-US02-29560-65 | Sequence 65, Appl |
| 23 | 504.6 | 28.6 | 1863 | 14 | US-10-245-882-65 | Sequence 65, Appl |
| 24 | 504.6 | 28.6 | 3926 | 11 | US-09-949-016-1224 | Sequence 1224, Ap |
| 25 | 504.6 | 28.6 | 3926 | 15 | US-10-170-235-27078 | Sequence 27078, A |
| 26 | 504.6 | 28.6 | 3945 | 14 | US-10-101-510-551 | Sequence 551, App |
| 27 | 504.6 | 28.6 | 3946 | 2 | PCT-US02-28859-53 | Sequence 53, Appl |
| 28 | 504.6 | 28.6 | 3946 | 11 | US-09-949-016-146 | Sequence 146, App |
| 29 | 504.6 | 28.6 | 3946 | 12 | US-09-968-007A-209 | Sequence 209, App |
| 30 | 504.6 | 28.6 | 3946 | 14 | US-10-241-220-53 | Sequence 53, Appl |
| 31 | 504.6 | 28.6 | 3946 | 14 | US-10-126-052A-508 | Sequence 508, App |
| 32 | 504.6 | 28.6 | 3946 | 16 | US-10-295-027-303 | Sequence 303, App |
| 33 | 504.6 | 28.6 | 3946 | 19 | US-60-471-729-12 | Sequence 12, Appl |
| 34 | 500 | 28.3 | 1828 | 14 | US-10-144-771-5193 | Sequence 5193, Ap |
| 35 | 488.4 | 27.7 | 2221 | 2 | PCT-US03-03482-3790 | Sequence 3790, Ap |
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| 37 | 464.4 | 26.3 | 3404 | 2 | PCT-US03-03194-3118 | Sequence 3118, Ap |
| 38 | 464.4 | 26.3 | 3404 | 15 | US-10-219-051B-14417 | Sequence 14417, A |
| 39 | 464.4 | 26.3 | 3404 | 18 | US-60-436-643-3118 | Sequence 3118, Ap |
| 40 | 456.4 | 25.9 | 3377 | 14 | US-10-144-771-5360 | Sequence 5360, Ap |
| 41 | 425.4 | 24.1 | 4056 | 14 | US-10-144-771-20704 | Sequence 20704, A |
| 42 | 424 | 24.0 | 1800 | 2 | PCT-US03-01450-6 | Sequence 6, Appli |
| 43 | 424 | 24.0 | 1800 | 14 | US-10-345-680-6 | Sequence 6, Appli |
| 44 | 424 | 24.0 | 2298 | 2 | PCT-US03-01450-4 | Sequence 4, Appli |
| 45 | 424 | 24.0 | 2298 | 14 | US-10-170-385-438 | Sequence 438, App |

ALIGNMENTS

RESULT 1
PCT-US02-08970-3
; Sequence 3, Application PC/TUS0208970
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as Novel
; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093800PC
; CURRENT APPLICATION NUMBER: PCT/US02/08970
; CURRENT FILING DATE: 2003-09-27
; PRIOR APPLICATION NUMBER: US 09/815,923
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: serotonin transporter
PCT-US02-08970-3

Query Match 100.0%; Score 1764; DB 2; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ACCGCTCAGAAAAGCCGTTCGGTGGTGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACC 120
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Qy       181 GTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTAC 240
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RESULT 2
US-10-144-771-11577
; Sequence 11577, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 11577
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-11577

Query Match 32.9%; Score 579.8; DB 14; Length 2745;
Best Local Similarity 59.8%; Pred. No. 1.2e-165;
Matches 989; Conservative 0; Mismatches 662; Indels 3; Gaps 1;

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Qy       206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
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Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642

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Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702

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Qy       1703 CAATCCAACGTCCGGAAGTGACGTCGATACCTCC 1736

Db       2017 AAAGTATCACTCCTGAAACACCAACGGAAATTCC 2050


RESULT 3
US-10-219-051B-13968
; Sequence 13968, Application US/10219051B
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 13968
;   LENGTH: 3190
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: EMBL / X63995
;   DATABASE ENTRY DATE: 1992-07-29
US-10-219-051B-13968

  Query Match             32.8%;  Score 579.4;  DB 15;  Length 3190;
  Best Local Similarity   60.0%;  Pred. No. 1.7e-165;
  Matches  983;  Conservative    0;  Mismatches  651;  Indels    3;  Gaps    1;

Qy          86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145

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Qy         146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205

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Qy         206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265

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Qy       386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
Db       669 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 728

Qy       446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
Db       729 CCCTCACGGACCGGCTGCCCTGGACTAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 788

Qy       506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
Db       789 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 848

Qy       566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
Db       849 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 908

Qy       626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
Db       909 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 968

Qy       686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
Db       969 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 1028

Qy       746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
Db      1029 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 1088

Qy       806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
Db      1089 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 1148

Qy       866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
Db      1149 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1208

Qy       926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
Db      1209 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1268

Qy       986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
Db      1269 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1328

Qy      1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
Db      1329 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1388

Qy      1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
Db      1389 ATGCAGAGGCAATAGCCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1448

Qy      1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
Db      1449 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1508

Qy      1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
Db      1509 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1568

Qy      1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
Db      1569 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1628

Qy      1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
Db      1629 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1688

Qy      1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
Db      1689 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1748

Qy      1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
Db      1749 GCTTCAGCCCGGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1808

Qy      1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
Db      1809 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1868

Qy      1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
Db      1869 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1928

Qy      1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
Db      1929 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGCATTATTA 1988

Qy      1703 CAATCCAACGTCCGGAA 1719
Db      1989 AAAGTATCACTCCTGAA 2005
```

RESULT 4
US-60-453-135-5294
; Sequence 5294, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5294
; LENGTH: 2964
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-5294

Query Match 31.5%; Score 554.8; DB 18; Length 2964;
Best Local Similarity 59.5%; Pred. No. 5.3e-158;
Matches 953; Conservative 2; Mismatches 644; Indels 3; Gaps 1;

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Qy       107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db       302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy       167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db       362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy       227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db       422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy       287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db       482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy       347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db       542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy       407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db       602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy       467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
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Db        662 GGACCAGCTGCAASAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586

Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646

Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706

Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766

Db        902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826

Db        962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886

Db       1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946

Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006

Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066

Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123

Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183

Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243

Db       1382 ACAGCACRTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303

Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363

Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423

Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483

Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTYGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543

Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603

Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663

Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705

Db       1862 TGATCATCACTCCAGGGACATTTAAMGAGCGTATTATTAAAA 1903


RESULT 5
US-60-453-050-5294
; Sequence 5294, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5294
;   LENGTH: 2964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-453-050-5294

  Query Match             31.5%;  Score 554.8;  DB 18;  Length 2964;
  Best Local Similarity   59.5%;  Pred. No. 5.3e-158;
  Matches  953;  Conservative    2;  Mismatches  644;  Indels    3;  Gaps    1;

Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166

Db        302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226

Db        362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286

Db        422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346

Db        482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406

Db        542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466

Db        602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526

Db        662 GGACCAGCTGCAASAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586

Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646

Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706

Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901
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Qy       707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db       902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy       767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db       962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy       827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
Db      1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy       887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
Db      1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy       947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
Db      1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201

Qy      1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
Db      1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy      1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
Db      1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy      1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
Db      1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy      1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
Db      1382 ACAGCACRTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy      1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
Db      1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy      1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
Db      1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy      1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
Db      1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy      1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
Db      1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTYGGCTTCAGCCCGGGGTGGTTCT 1681

Qy      1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
Db      1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy      1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
Db      1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy      1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
Db      1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy      1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
Db      1862 TGATCATCACTCCAGGGACATTTAAMGAGCGTATTATTAAAA 1903

RESULT 6
US-60-466-412-5294
; Sequence 5294, Application US/60466412

; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001466
;  CURRENT APPLICATION NUMBER: US/60/466,412
;  CURRENT FILING DATE:  2003-04-30
;  NUMBER OF SEQ ID NOS: 429241
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5294
;   LENGTH: 2964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-466-412-5294

  Query Match             31.5%;  Score 554.8;  DB 19;  Length 2964;
  Best Local Similarity   59.5%;  Pred. No. 5.3e-158;
  Matches  953;  Conservative    2;  Mismatches  644;  Indels    3;  Gaps    1;

Qy       107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db       302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy       167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db       362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy       227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db       422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy       287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db       482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy       347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db       542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy       407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db       602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy       467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
Db       662 GGACCAGCTGCAASAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy       527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
Db       722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy       587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
Db       782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy       647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
Db       842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy       707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db       902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy       767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db       962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy       827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
Db      1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy       887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
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Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006

Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066

Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123

Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183

Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243

Db       1382 ACAGCACRTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303

Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363

Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423

Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483

Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTYGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543

Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603

Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663

Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705

Db       1862 TGATCATCACTCCAGGGACATTTAAMGAGCGTATTATTAAAA 1903


RESULT 7
US-10-219-051B-13970
; Sequence 13970, Application US/10219051B
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 13970
;   LENGTH: 2508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: EMBL / L05568
;   DATABASE ENTRY DATE: 2000-03-04
US-10-219-051B-13970

  Query Match             31.3%;  Score 552.4;  DB 15;  Length 2508;
  Best Local Similarity   59.5%;  Pred. No. 2.6e-157;
  Matches  953;  Conservative    0;  Mismatches  646;  Indels    3;  Gaps    1;

Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166

Db        302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226

Db        362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286

Db        422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346

Db        482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406

Db        542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466

Db        602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526

Db        662 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586

Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646

Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706

Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766

Db        902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826

Db        962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886

Db       1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946

Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006

Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201
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Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
             | ||||| ||| | ||  | || ||||||||  |  |   |||  |      |    ||||
Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
             | | |     || ||| ||  | ||  | ||||||  |||  | || || || |||| ||
Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
             || | |  |||   ||||  ||||||||||||| || ||| | || || ||||  | |
Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
             |||| || |||| ||  | ||||  || | ||||||| |    || || |  || |  |
Db       1382 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
             | |  | ||  |  || ||    || |||   |   || | |   |  ||   || |
Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
             | |||  ||||   || |  || || |  ||| | ||  | || ||  | | ||||| |
Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
             | ||    ||  | ||    || |   |    || || | ||  |||  ||| | ||||
Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
             || ||   | ||||     || |||| |   ||||| ||   || ||| || |||||||
Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
             ||||||  ||| |||     |||||| ||  |  ||  | ||| |  |  |       |
Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
             |  ||   |       |  | |         |||| |  |||||  |  |||  ||||| |
Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
             | || |     ||      | |  |  ||  ||||| ||    ||  ||    ||
Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
             || |||||||||| || |  |  |  | || || |  | ||
Db       1862 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 1903
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RESULT 8
PCT-US02-39565-43
; Sequence 43, Application PC/TUS0239565
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: CHIEN, David
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: GORVAD, Ann E.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: HAWKINGS, Philip R.
; APPLICANT: JACKSON, Alan P.
; APPLICANT: JIANG, Xin
; APPLICANT: JIN, Pei
; APPLICANT: KABLE, Amy E.
; APPLICANT: KHARE, Reena
; APPLICANT: LAL, Preeti G.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: LEE, Sally
; APPLICANT: LEE, Soo Yeun
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: REDDY, Roopa
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: RING, Huijun Z.
; APPLICANT: SPRAGUE, William W.
; APPLICANT: SWARNAKR, Anita
; APPLICANT: TANG, Y. Tom
; APPLICANT: ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-1336 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/39565
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/340,741
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/351,359
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/359,506
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PERL Program
; SEQ ID NO 43
; LENGTH: 2770
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7508471CB1
PCT-US02-39565-43

Query Match 31.3%; Score 552.4; DB 2; Length 2770;
Best Local Similarity 59.5%; Pred. No. 2.8e-157;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

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Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
              || | || |||||||||||  |||||||  || |||||  ||  | ||| | || |  || |
Db        552 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 611

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
              |||| || || || || ||||| |||||||||||| |||||||||||||||| || || |
Db        612 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 671

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
              |||| |||| ||| | | |||     | ||||| ||  | ||||| || | | |||| |
Db        672 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 731

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
              | || ||||| ||||||||||     || ||| |  |  | ||||     ||||||||
Db        732 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 791

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
                | |||||  | || ||||||||||||||| || | | | ||||| |     |||||||
Db        792 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 851

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
              |||| ||||| |  |||||| | || ||||| ||| | ||  ||  ||          |
Db        852 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 911

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
              |      || |  | || |   |||    | |||     |     |.|    | |    |
Db        912 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 971

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
                      |  |   | ||  |  | || ||  | || || | |   ||  | ||
Db        972 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 1031

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
              || ||   |||  |||||| || ||  | ||| |||||   ||||    | ||||| |
Db       1032 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 1091

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
              | ||  |  |   | ||||     |  |||||||  | | ||||||| |||| ||
Db       1092 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 1151
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Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db       1152 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 1211

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db       1212 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1271

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
Db       1272 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1331

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
Db       1332 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1391

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
Db       1392 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1451

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
Db       1452 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1511

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
Db       1512 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1571

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
Db       1572 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1631

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
Db       1632 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1691

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
Db       1692 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1751

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
Db       1752 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1811

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
Db       1812 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1871

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
Db       1872 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1931

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
Db       1932 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1991

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
Db       1992 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 2051

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
Db       2052 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 2111

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
Db       2112 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 2153

RESULT 9
US-09-949-016-3430
; Sequence 3430, Application US/09949016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3430
;   LENGTH: 2964
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3430

  Query Match             31.3%;  Score 552.4;  DB 11;  Length 2964;
  Best Local Similarity   59.5%;  Pred. No. 2.9e-157;
  Matches  953;  Conservative    0;  Mismatches  646;  Indels    3;  Gaps    1;

Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db        302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db        362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db        422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db        482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db        542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db        602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
Db        662 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db        902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db        962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
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Db       1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
              | ||||| || || ||   ||| |||||  |  | ||||||||||||||||||||||||
Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
              |||||   || || ||  | ||        | |||||| |||| |||||| || | || |
Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
              | ||||| ||| | ||  | || ||||||||  |  |  ||| |     |    ||||
Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
              | | |     || ||| ||  | ||  | ||||||  |||  | || || || |||| ||
Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
              || | |  |||   ||||  |||||||||||||| || ||| | || || |||||  | |
Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
              |||| || |||| |||  | ||||  || | |||||||  |    || || |  || |  |
Db       1382 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
              | |  | ||  |  || ||    || |||   |  || |   |   ||   || |
Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
              | |||  ||||   || |  || || |  ||| | ||  | || ||  | | |||||  |
Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
              | ||    ||  | ||    || |  |    || || | ||  |||  ||| | ||||
Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
              || ||   | |||||     || |||| |   ||||| ||   || ||| || |||||||
Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
              |||||| ||| |||    .||||||  ||  | ||  | ||| |  |  |        |
Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
              |  ||   |      |  | |          |||| |  ||||| |  |||  ||||| |
Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
              | || |     ||      | |  |  ||   ||||| ||    || ||    ||
Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
              || |||||||||| || |  |  |   | || || |  | ||
Db       1862 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 1903


RESULT 10
US-10-170-235-38741
; Sequence 38741, Application US/10170235
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
;  TITLE OF INVENTION:  TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
;  FILE REFERENCE: CL001380
;  CURRENT APPLICATION NUMBER: US/10/170,235
;  CURRENT FILING DATE:  2003-03-17
;  NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 38741
;   LENGTH: 2964
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-38741

  Query Match             31.3%;  Score 552.4;  DB 15;  Length 2964;
  Best Local Similarity   59.5%;  Pred. No. 2.9e-157;
  Matches  953;  Conservative    0;  Mismatches  646;  Indels    3;  Gaps    1;

Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
              || | || ||||||||||  |||||||  || |||||  ||  | ||| | || |  || |
Db        302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
              ||||  || || ||  || ||||| ||||||||||| |||||||||||||||||  || || |
Db        362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
              ||||  |||| |||  | |.|||    | |||||  ||  | |||||  || | | |||| |
Db        422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
              | || |||||  ||||||||||    || ||| |  |  | ||||     |||||||
Db        482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
                | |||||  | || ||||||||||||||| || | | | |||||  |     |||||||
Db        542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
              |||| |||||  |  ||||||  | || |||||  ||| | ||  || ||          |
Db        602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
              |       || |  | || |   |||    | |||   |  |  |    |     |
Db        662 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
                        |  |   | || |  | || ||  | ||  | | |   ||  | ||
Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
              || ||   |||  |||||| || ||  | ||| |||||   ||||    | ||||||  |
Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
              | ||  |  |   | ||||     | ||||||||  | | |||||||| |||| ||
Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
              ||||||||||||||||||||||||||      ||| ||  |  | ||   | |||||||
Db        902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
              |||  || | ||| || || |||||    |  |||  |  | ||  |||| | |  ||  | |
Db        962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
              |||| ||| | |    |  |   ||| ||||| || || ||  | ||||| |||||||  |
Db       1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
              | ||||| || || ||   ||| |||||  |  | ||||||||||||||||||||||||
Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
              |||||   || || ||  | ||        | |||||| |||| |||||| || | || |
Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
              | ||||| ||| | ||  | || ||||||||  |  |  ||| |     |    ||||
Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
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Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183

Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243

Db       1382 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303

Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363

Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423

Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483

Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543

Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603

Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663

Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705

Db       1862 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 1903
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RESULT 11
US-60-453-135-1580
; Sequence 1580, Application US/60453135
; GENERAL INFORMATION:
  APPLICANT: CARGILL, Michele
  APPLICANT:  IAKOUBOVA, Olga
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001456
;  CURRENT APPLICATION NUMBER: US/60/453,135
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1580
;   LENGTH: 2342
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-453-135-1580

  Query Match             29.7%;  Score 524;  DB 18;  Length 2342;
  Best Local Similarity   59.4%;  Pred. No. 1.2e-148;
  Matches  948;  Conservative   12;  Mismatches  612;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162

Db        412 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCRTAGTCGGCTTC 471

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222

Db        472 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 531

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282

Db        532 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 591

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342

Db        592 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 648

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402

Db        649 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 708

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC----------TCTC 450

Db        709 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 768

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509

Db        769 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 828

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564

Db        829 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 888

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624

Db        889 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 948

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684

Db        949 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCRTCATCGTCTTGTATTTTAGC 1008

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744

Db       1009 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 1068

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804

Db       1069 TTCGTGCTGTTCGTGCTCCTGGTSCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 1128

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864

Db       1129 AMTGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 1188

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924

Db       1189 GCAACTCAGATATTTTTTTCCYTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 1248

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984

Db       1249 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1308

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044

Db       1309 ATCACCAGCTTCSTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGSCCCATGAA 1368

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104

Db       1369 CACAAGGTCARCATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1428

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164

Db       1429 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1488

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224

Db       1489 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACRGGCCTG 1548

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284

Db       1549 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCRTCACC 1605
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Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
Db       1606 TTCAGCACTTTCCTTCTCSCCCTGTTCTGCATAACCARGGGTGGAATTTACGTCTTGACC 1665

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
Db       1666 CTCCTGGACACCTTTGCTGCGRGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1725

Qy       1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
Db       1726 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1785

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
Db       1786 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTKCCTCCTG 1845

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584
Db       1846 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACYACATCTTC 1905

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644
Db       1906 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1965

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680
Db       1966 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 2001


RESULT 12
US-60-453-050-1580
; Sequence 1580, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1580
;   LENGTH: 2342
;   TYPE: DNA
;   ORGANISM: Homo sapiens
60-453-050-1580

  Query Match             29.7%;  Score 524;  DB 18;  Length 2342;
  Best Local Similarity   59.4%;  Pred. No. 1.2e-148;
  Matches  948;  Conservative   12;  Mismatches  612;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
Db        412 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCRTAGTCGGCTTC 471

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
Db        472 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 531

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
Db        532 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 591

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342
Db        592 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 648

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402
Db        649 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 708

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC----------TCTC 450
Db        709 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 768

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509
Db        769 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 828

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564
Db        829 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 888

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624
Db        889 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 948

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684
Db        949 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCRTCATCGTCTTGTATTTTAGC 1008

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744
Db       1009 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 1068

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804
Db       1069 TTCGTGCTGTTCGTGCTCCTGGTSCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 1128

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864
Db       1129 AMTGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 1188

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924
Db       1189 GCAACTCAGATATTTTTTTCCYTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 1248

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984
Db       1249 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1308

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044
Db       1309 ATCACCAGCTTCSTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGSCCCATGAA 1368

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104
Db       1369 CACAAGGTCARCATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1428

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164
Db       1429 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1488

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224
Db       1489 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACRGGCCTG 1548

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284
Db       1549 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCRTCACC 1605

Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
Db       1606 TTCAGCACTTTCCTTCTCSCCCTGTTCTGCATAACCARGGGTGGAATTTACGTCTTGACC 1665

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
Db       1666 CTCCTGGACACCTTTGCTGCGRGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1725

Qy       1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
Db       1726 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1785

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
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Db       1786 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTKCCTCCTG 1845

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584

Db       1846 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACYACATCTTC 1905

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644

Db       1906 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1965

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680

Db       1966 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 2001


RESULT 13
US-60-466-412-1580
; Sequence 1580, Application US/60466412
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001466
;  CURRENT APPLICATION NUMBER: US/60/466,412
;  CURRENT FILING DATE:  2003-04-30
;  NUMBER OF SEQ ID NOS: 429241
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1580
;   LENGTH: 2342
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-466-412-1580

  Query Match             29.7%;  Score 524;  DB 19;  Length 2342;
  Best Local Similarity   59.4%;  Pred. No. 1.2e-148;
  Matches  948;  Conservative   12;  Mismatches  612;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162

Db        412 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCRTAGTCGGCTTC 471

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222

Db        472 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 531

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282

Db        532 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 591

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342

Db        592 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 648

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402

Db        649 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 708

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC----------TCTC 450

Db        709 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 768

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509

Db        769 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 828

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564

Db        829 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 888

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624

Db        889 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 948

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684

Db        949 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCRTCATCGTCTTGTATTTTAGC 1008

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744

Db       1009 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 1068

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804

Db       1069 TTCGTGCTGTTCGTGCTCCTGGTSCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 1128

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864

Db       1129 AMTGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 1188

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924

Db       1189 GCAACTCAGATATTTTTTTCCYTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 1248

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984

Db       1249 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1308

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044

Db       1309 ATCACCAGCTTCSTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGSCCCATGAA 1368

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104

Db       1369 CACAAGGTCARCATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1428

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164

Db       1429 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1488

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224

Db       1489 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACRGGCCTG 1548

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284

Db       1549 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCRTCACC 1605

Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344

Db       1606 TTCAGCACTTTCCTTCTCSCCCTGTTCTGCATAACCARGGGTGGAATTTACGTCTTGACC 1665

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404

Db       1666 CTCCTGGACACCTTTGCTGCGRGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1725

Qy       1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464

Db       1726 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1785

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524

Db       1786 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTKCCTCCTG 1845

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584

Db       1846 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACYACATCTTC 1905

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644

Db       1906 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1965

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680

Db       1966 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 2001
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RESULT 14
US-10-219-051B-3166
; Sequence 3166, Application US/10219051B
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
;  SEQ ID NO 3166
;    LENGTH: 1983
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;    DATABASE ACCESSION NUMBER: EMBL / M65105
;    DATABASE ENTRY DATE: 2000-03-04
US-10-219-051B-3166

  Query Match             29.6%;  Score 522.4;  DB 15;  Length 1983;
  Best Local Similarity   59.9%;  Pred. No. 3.5e-148;
  Matches  956;  Conservative    0;  Mismatches  616;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
              |||| ||  || ||||||||||  ||||||   || |||||||| | || || || |||
Db        217 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCGTAGTCGGCTTC 276

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
              |||||||| || |  |||||||||||| |||||||| |||| ||| |||| || ||||||
Db        277 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 336

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
              || ||| ||||||||||     | || |  | | | ||| |||| ||||||| | ||
Db        337 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 396

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342
              || ||||| ||||| |||||| ||||    ||       |||  | ||||||   ||||||
Db        397 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 453

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402
              ||     | ||||| || |||||||  ||  | ||||||  | | ||| | ||| | |||
Db        454 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 513

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC----------TCTC 450
              ||||||  |||||||  ||| |  | || ||||  || | ||           ||
Db        514 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 573

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509
                | |  |   ||| ||  |   | |||| ||||  | ||           || ||  ||
Db        574 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 633

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564
                  | |  ||  | || |    |  ||          ||   |  || |||||
Db        634 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 693

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624
              |||||  |  || |||  |||  || | |  ||| ||   | |||  |  |||||| ||
Db        694 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 753

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684
              | |  | ||  |  |||    || ||| || | |  ||| |  || || | || ||  |
Db        754 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCGTCATCGTCTTGTATTTTAGC 813

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744
              | ||||||||  || | ||   | || ||||||||||| | |||||   |   || |||
Db        814 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 873

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804
              | |||||| |  | || ||||     |||||||||||| || |||||  |  | |||||
Db        874 TTCGTGCTGTTCGTGCTCCTGGTCCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 933

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864
                  ||||||  |   || |   ||   ||| || |  | | ||||||||||| ||
Db        934 AATGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 993

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924
              ||| | ||||| || || ||  | ||  | || || |||    |  | ||  |  ||||
Db        994 GCAACTCAGATATTTTTTCCTTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 1053

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984
              |||||||| ||  |||||||||| |||||||| || ||  | ||       ||||||||
Db       1054 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1113

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044
              | |||||||||  |  |||| |||| ||| |||||  |  | || ||||||||  || |
Db       1114 ATCACCAGCTTCGTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGGCCCATGAA 1173

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104
              || ||    | ||| ||||| || | |   |||||  ||| || ||||||||| ||||
Db       1174 CACAAGGTCAACATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1233

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164
              || |||||||  | ||| || | || ||    |||||||  |  | || ||| |||||
Db       1234 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1293

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224
              ||  |  | ||||| |||||||  |  | |||||  | |||||  |||| |||||  ||
Db       1294 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACGGGCCTG 1353

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284
                 || || |    |  ||  |    |||| ||  || | ||     ||   |
Db       1354 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCGTCACC 1410

Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
              |   ||  |   ||  ||| ||| |  ||  ||  | ||||  | ||| || |   |
Db       1411 TTCAGCACTTTCCTTCTCGCCCTGTTCTGCATAACCAAGGGTGGAATTTACGTCTTGACC 1470

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
              || ||  |    | ||   | ||    | || || || |  ||   |   || ||   |
Db       1471 CTCCTGGACACCTTTGCTGCGGGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1530

Qy       1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
              || || | |||| | ||||| || ||| |||||    | ||  |   |  ||| |||||
Db       1531 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1590

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
                ||  || ||    | ||||||    || |||   | | |||||||  |  ||| | |||
Db       1591 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTTCCTCCTG 1650

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584
              | || | ||| ||  | |  |    | ||    |  |  ||  || |||| ||
Db       1651 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACTACATCTTC 1710

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644
              ||  | ||| | | |   || || ||||  ||  ||    || || |        | ||
Db       1711 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1770

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680
              | ||| | ||||| ||  | |||| ||| |  |||
Db       1771 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 1806


RESULT 15
US-10-219-051B-10901
; Sequence 10901, Application US/10219051B
; GENERAL INFORMATION:
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;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 10901
;   LENGTH: 1983
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: EMBL / M65105
    DATABASE ENTRY DATE: 2000-03-04
   10-219-051B-10901

  Query Match             29.6%;  Score 522.4;  DB 15;  Length 1983;
  Best Local Similarity   59.9%;  Pred. No. 3.5e-148;
  Matches  956;  Conservative    0;  Mismatches  616;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
              |||| ||  || |||||||||  ||||||   || |||||||| | || || || |||
Db        217 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCGTAGTCGGCTTC 276

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
              |||||||| || |  |||||||||| |||||||| |||| ||| |||| || ||||||
Db        277 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 336

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
              || ||| |||||||||||    |  | ||  |  | |  ||| |||| ||||||| | ||
Db        337 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 396

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342
              || ||||| ||||| |||||| ||||    ||       ||| | ||||||   ||||||
Db        397 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 453

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402
              ||      | ||||| || |||||||  ||  | |||||| | | ||| | ||| | |||
Db        454 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 513

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC------------TCTC 450
              ||||||   |||||||  ||| |  | || |||||  || | ||             ||
Db        514 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 573

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509
              | | |   ||| ||  |   | |||| ||||  | ||           || ||  ||
Db        574 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 633

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564
                  | |  ||  | || |    |  ||          ||   |  || |||||
Db        634 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 693

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624
              |||||  |  || |||  |||  || | |  ||| ||   | |||  |  |||||||  ||
Db        694 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 753

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684
              | |  | ||  |  |||    || ||| || | |  ||| |  || || | || ||   |
Db        754 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCGTCATCGTCTTGTATTTTAGC 813

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744
              | |||||||| || | ||   | || ||||||||||||| | |||||   |   || |||
Db        814 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 873

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804
              | |||||| |  | || ||||     |||||||||| || |||||  |  | |||||

Db        874 TTCGTGCTGTTCGTGCTCCTGGTCCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 933

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864
                  ||||||   |   || |  ||  ||| || |  | | ||||||||||||| ||
Db        934 AATGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 993

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924
              ||| | ||||| || || ||  | ||  | || || |||     |  | ||  |  ||||
Db        994 GCAACTCAGATATTTTTTTCCTTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 1053

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984
              |||||||| ||  |||||||||| |||||||| || ||  | ||       ||||||||
Db        1054 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1113

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044
              | |||||||||  |  |||| |||| ||| |||||  |  | || ||||||||  || |
Db        1114 ATCACCAGCTTCGTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGGCCCATGAA 1173

Qy        1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104
               || ||     | ||| ||||| || | |   |||||  |||| || |||||||| ||||
Db        1174 CACAAGGTCAACATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1233

Qy        1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164
               || ||||||||  | ||| || | || ||    ||||||||  |  | || ||| |||||
Db        1234 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1293

Qy        1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224
               ||  |  | |||||  |||||||  |  | |||||  | |||||  |||| |||||  ||
Db        1294 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACGGGCCTG 1353

Qy        1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284
                 || ||  |      |  ||  |      |||| ||  ||  | ||       ||   |
Db        1354 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCGTCACC 1410

Qy        1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
               |   ||  |   ||  ||| |||  |  ||  ||  | |||||  | ||| || |  |
Db        1411 TTCAGCACTTTCCTTCTCGCCCTGTTCTGCATAACCAAGGGTGGAATTTACGTCTTGACC 1470

Qy        1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
               || ||  |    | ||  | ||      | || || || |  ||  |    || ||   |
Db        1471 CTCCTGGACACCTTTGCTGCGGGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1530

Qy        1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
               || ||  | |||| | ||||| || ||| |||||     | ||  |   |   ||| |||||
Db        1531 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1590

Qy        1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
               ||  || ||    | ||||||    || |||   | | ||||||| |  ||| | |||
Db        1591 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTTCCTCCTG 1650

Qy        1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584
               |  || | ||| ||  | |  |       | ||     |   |  ||  || |||| ||
Db        1651 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACTACATCTTC 1710

Qy        1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644
               ||  | ||| | | |   || || |||  ||  ||    || || |         | ||
Db        1711 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1770

Qy        1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680
               | ||| | ||||| ||  | |||| ||| |  |||
Db        1771 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 1806


Search completed: July 18, 2003, 16:59:29
Job time : 1005 secs
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